

MET SER LEU LEU THR GLU VAL GLU THR PRO ILE
A T G A G C C T T C T A A C C G A G G T C G A A A C . . . A C C T A T
T A C T C G G A A G A T T G G C T C C A G C T T T G . . . T G G A T A
10 20 720

ARG ASN GLU TRP GLU CYS ARG CYS ASN GLY
C A G A A A C G A A T G G G A G T G C A G A T G C A A C G G
G T C T T T G C T T A C C C T C A C G T C T A C G T T G C C
730 740 750

SER SER ASP PRO LEU VAL VAL ALA ALA SER
T T C A A G T G A C C C G C T T G T T G T T G C T G C G A G
A A G T T C A C T G G G C G A A C A A C A A C G A C G C T C
760 770 780

ILE ILE GLY ILE LEU HIS LEU ILE LEU TRP
T A T C A T T G G G A T C T T G C A C T T G A T A T T G T G
A T A G T A A C C C T A G A A C G T G A A C T A T A A C A C
790 800 810

ILE PHE ASP ARG LEU PHE PHE LYS CYS ILE
G A T T T T T G A T C G T C T T T T T T T C A A A T G C A T
C T A A A A A C T A G C A G A A A A A A A G T T T A C G T A
820 830 840

TYR ARG LEU PHE LYS TYR GLY LEU LYS ARG
C T A T C G A C T C T T C A A A T A C G G T C T G A A A A G
G A T A G C T G A G A A G T T T A T G C C A G A C T T T T C
850 860 870

GLY PRO SER THR GLU GLY VAL PRO GLU SER
A G G G C C T T C T A C G G A A G G A G T A C C T G A G T C
T C C C G G A A G A T G C C T T C C T C A T G G A C T C A G
880 890 900

MET ARG GLU GLU TYR ARG LYS GLU GLN GLN
T A T G A G G G A A G A A T A T C G A A A G G A A C A G C A
A T A C T C C C T T C T T A T A G C T T T C C T T G T C G T
910 920 930

ASN ALA VAL ASP ALA ASP ASP SER HIS PHE
G A A T G C T G T G G A T G C T G A C G A C A G T C A T T T
C T T A C G A C A C C T A C G A C T G C T G T C A G T A A A
940 950 960

VAL SER ILE GLU LEU GLU ***
T G T C A G C A T A G A G C T G G A G T A A
A C A G T C G T A T C T C G A C C T C A T T
970 980

Figure 2

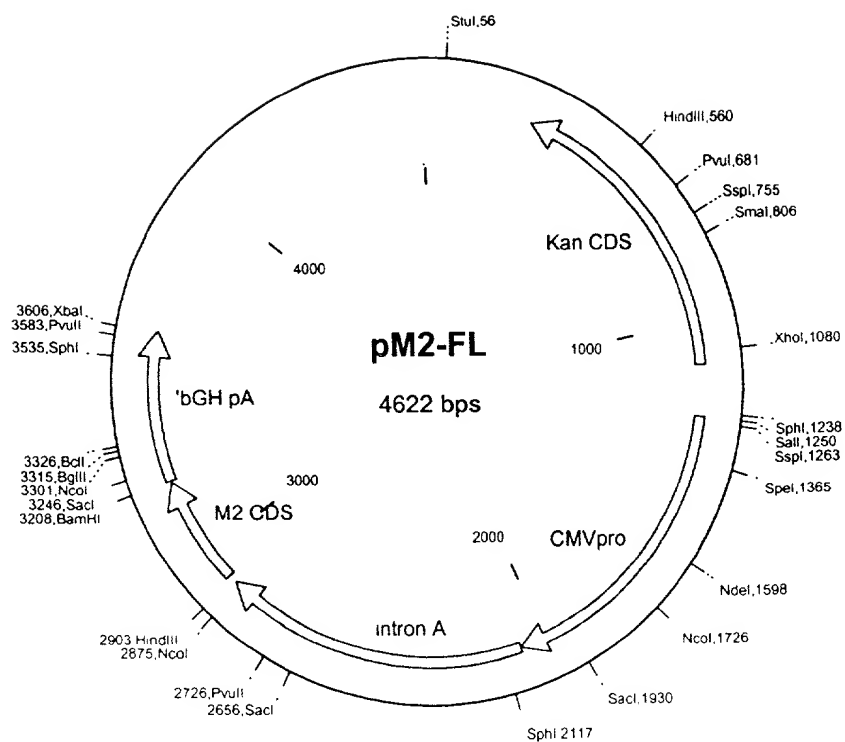


Figure 3

1 GGGGGGGGGG GCGCTGAGG TCTGCCTCGT GAAGAAGGTG TTGCTGACTC ATACCAGGCC TGAATCGCCC CATCATCCAG CCAGAAAAGTG
 91 AGGGAGCCAC GGTGATGAG AGCTTTGTTG TAGTGGGACC AGTTGGTGAT TTTGAACTTT TGCTTTGCCA CGGAACGGTC TCGTTGTGCG
 181 GGAAGATGCG TGATCTGATC CTTCACCTCA GCAAAAGTTC GATTATTCA ACAAGCCGC CGTCCCGTCA AGTCAGCGTA ATGCTCTGCC
 271 AGTGTACAA CCAATTAACC AATTCTGATT AGAAAACTC ATCGAGCATC AAATGAACT GCAATTATT CATATCAGGA TTATCAATAC
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 361 CATATTTTGG AAAAAGCCGT TTCTGTAATG AAGGAGAAAA CTCACCGAGG CAGTTCCATA GGATGGCAAG ATCTGGTAT CGGTCTGCGA
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 451 TTCCGACTCG TCCAACATCA ATACAACCTA TTAATTTCCC CTGTCAAAA ATAAGGTTAT CAAGTGAGAA ATCACCATGA GTGACGACTG
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 <Kan CDS.....<
 631 CAACCAAACC GTTATTCATT CGTGATTGCG CCTGAGCGAG ACGAAATACG CGATCGCTGT TAAAAGGACA ATTACAAACA GGAATCGAAT
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 721 GCAACCGGCG CAGGAACACT GCCAGCGCAT CAACATATT TTCACCTGAA TCAGGATATT CTTCTAATAC CTGGAATGCT GTTTTCCCGG
 <Kan CDS.....<
 811 GGATCGCAGT GGTGAGTAAC CATGCATCAT CAGGAGTACG GATAAAATGC TTGATGGTCG GAAGAGGCAT AAATTCGCTC AGCCAGTTTA
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 901 GTCTGACCAT CTCATCTGTA ACATCATTTG CAACGCTACC TTTGCCATGT TTCAGAAACA ACTCTGGCGC ATCGGGCTTC CCATACAATC
 <Kan CDS.....<
 991 GATAGATTGT CGCACCTGAT TGCCCGACAT TATCGCGAGC CCATTTATAC CCATATAAAT CAGCATCCAT GTTGGAATTT AATCGCGGCC
 <Kan CDS.....<
 1081 TCGAGCAAGA CGTTTCCCGT TGAATATGGC TCATAACACC CTTGTATTA CTGTTTATGT AAGCAGACAG TTTTATGTT CATGATGATA
 <Kan CDS.....<
 1171 TATTTTATC TTGTGCAATG TAACATCAGA GATTTTGAGA CACAACGTGG CTTTCCCCC CCCCCGGCA TGCCTGCAGG TCGACATAAA
 >>CMVpro >
 1261 TCAATATTGG CTATTGGCCA TTGCATACGT TGTATCTATA TCATAATATG TACATTTATA TTGGCTCATG TCCAATATGA CCGCATGTT
 >CMVpro.....>
 1351 GACATTGATT ATTGACTAGT TATTAATAGT AATCAATTAC GGGGTCATTA GTTCATAGCC CATATATGGA GTTCCGCGTT ACATAACTTA
 >CMVpro.....>
 1441 CGGTAAATGG CCCGCTCGT GACCGCCCAA CGACCCCGC CCATTGACGT CAATAATGAC GTATGTTCCC ATAGTAACGC CAATAGGGAC
 >CMVpro.....>
 1531 TTTCCATTGA CGTCAATGGG TGGAGTATTT ACGGTAAACT GCCCACTTGG CAGTACATCA AGTGATCAT ATGCCAAGTC CGGCCCCCTA
 >CMVpro.....>
 1621 TTGACGTCAA TGACGGTAAA TGGCCCGCCT GGCATTATGC CCAGTACATG ACCTTACGGG ACTTTCCTAC TTGGCAGTAC ATCTACGTAT
 >CMVpro.....>
 1711 TAGTCATGCG TATTACCATG GTGATCGCGT TTTGGCAGTA CACCAATGGG CGTGGATAGC GGTGAGTAC ACGGGGATTT CCAAGTCTCC
 >CMVpro.....>
 1801 ACCCCATTGA CGTCAATGGG AGTTTGTGTT GGCACCAAAA TCAACGGGAC TTCCAAAAT GTCGTAATAA CCCCCCCCCG TTGACGCAAA
 >CMVpro.....>

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1891 TGGGCGGTAG GCGTGTACGG TGGGAGGTCT ATATAAGCAG AGCTCGTTTA GTGAACCGTC AGATCGCCTG GAGACGCCAT CCACGCTGTT
>CMVpro.>

1981 TTGACCTCCA TAGAAGACAC CGGGACCGAT CCAGCCTCCG CGGCCGGGAA CGGTGCATTG GAACGCGGAT TCCCCGTGCC AAGAGTGAAG
>CMVpro.....>>

2071 TAAGTACCGC CTATAGACTC TATAGGCACA CCCCTTTGGC TCTTATGCAT GCTATACTGT TTTTGGCTTG GGGCCTATAC ACCCCGCTC
>intron A.....>

2161 CTTATGCTAT AGGTGATGGT ATAGCTTAGC CTATAGGTGT GGGTATTGA CCATTATTGA CCACTCCCCT ATTGGTGAGC ATACTTTCCA
>intron A.....>

2251 TTACTAATCC ATAACATGGC TCTTTGCCAC AACTATCTCT ATTGGCTATA TGCCAATACT CTGTCCTTCA GAGACTGACA CGGACTCTGT
>intron A.....>

2341 ATTTTACAG GATGGGGTCC CATTATTAT TTACAAATC ACATATACAA CAACGCCGTC CCCCCTGCCC GCAGTTTTTA TTAACATAG
>intron A.....>

2431 CGTGGGATCT CCACGCGAAT CTCGGGTACG TGTCCGGAC ATGGGCTCTT CTCCGTAGC GCGGAGCTT CCACATCCGA GCCCTGGTC
>intron A.....>

2521 CATGCCTCCA GCGGCTCATG GTCGCTCGC AGTCCTTGC TCCTAACAGT GGAGGCCAGA CTTAGGCACA GCACAATGCC CACCACCACC
>intron A.....>

2611 AGTGTGCCG ACAAGGCCGT GCGGGTAGGG TATGTGTCTG AAAATGAGCT CGGAGATTGG GCTCGCACC TGACGCAGAT GGAAGACTTA
>intron A.....>

2701 AGGCAGCGC AGAAGAAGAT GCAGGCAGCT GAGTTGTGT ATTCTGATAA GAGTCAGAG TAACCTCCGT TCGGTGCTG TTAACGTGG
>intron A.....>

2791 AGGGCAGTGT AGTCTGAGCA GTACTCGTTG CTGCCGCGC CGCCACCAGA CATAATAGCT GACAGACTAA CAGACTGTTC CTTCCATGG
>intron A.....>

2881 GTCTTTTCTG CAGTCACCGT CCAAGCTTCC ACCATGAGCC TTCTAACCGA GGTGAAACA CCTATCAGAA ACGAATGGGA GTGCAGATGC
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2971 AACGGTTCAA GTGACCCGCT TGTGTGTGCT GCGAGTATCA TTGGGATCTT GCACTTGATA TTGTGGATT TTGATCGTCT TTTTTCAAA
>M2 CDS.....>

3061 TGCATCTATC GACTCTTCAA ATACGGTCTG AAAAGAGGGC CTCTACGGA AGGAGTACCT GAGTCTATGA GGAAGAATA TCGAAAGGAA
>M2 CDS.....>

3151 CAGCAGAATG CTGTGGATGC TGACGACAGT CATTTTGTCA GCATAGAGCT GGAGTAAGGA TCCTCGCAAT CCCTAGGAGG ATTAGGCAAG
>M2 CDS.....>>bGH pA.....>

3241 GGCTTGAGCT CACGCTCTTG TGAGGGACAG AAATACAATC AGGGGCAGTA TATGAATACT CCATGGAGAA ACCCAGATCT ACGTATGATC
>bGH pA.....>

3331 AGCCTCGACT GTGCCTTCTA GTTGCCAGCC ATCTGTTGTT TGCCCTCCC CCGTGCCTTC CTTGACCCTG GAAGGTGCCA CTCCTACTGT
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3421 CTTTCTTAA TAAATGAGG AAATTGCATC GCATTGTCTG AGTAGGTGTC ATTCTATTCT GGGGGTGGG GTGGGGCAGG ACAGCAAGGG
>bGH pA.....>

3511 GGAGGATTGG GAAGACAATA GCAGGCATGC TGGGGATGCG GTGGGCTCTA TGCTTCTGA GCGGAAAGA ACCAGCTGGG GCTCGACAGC
>bGH pA.....>

3601 TCGACTCTAG AATTGCTTCC TCGCTCACTG ACTCGCTGCG CTCGTCGTT CGGCTGCGC GAGCGGTATC AGCTCACTCA AAGGCGGTAA
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4051 AACCCCCCGT TCAGCCCGAC CGTGGCGCTT TATCCGATA CTATCGTCTT GAGTCCAACC CGGTAAGACA CGACTTATCG CCACTGGCAG
4141 CAGCCACTGG TAACAGGATT AGCAGAGCGA GGTATGTAGG CGGTGCTACA GAGTCTTGA AGTGGTGGCC TAACTACGGC TAACTAGAA
4231 GGACAGTATT TGGTATCTGC GCTCTGCTGA AGCCAGTTAC CTTGGAAAA AGAGTTGGTA GCTCTTGATC CGGCAAAACA ACCACCGCTG
4321 GTAGCGGTGG TTTTTTTGTT TGCAAGCAGC AGATTACGCG CAGAAAAAAA GGATCTCAAG AAGATCCTTT GATCTTTTCT ACGGGGTCTG
4411 ACGCTCAGTG GAACGAAAAC TCACGTAAAG GGATTTTGGT CATGAGATTA TCAAAAAGGA TCTTCACCTA GATCCTTTTA AATTAAAAAT
4501 GAAGTTTAA ATCAATCTAA AGTATATATG AGTAACTTG GTCTGACAGT TACCAATGCT TAATCAGTGA GGCACCTATC TCAGCGATCT
4591 GTCTATTTTC TTCATCCATA GTTGCCTGAC TC

Figure 4

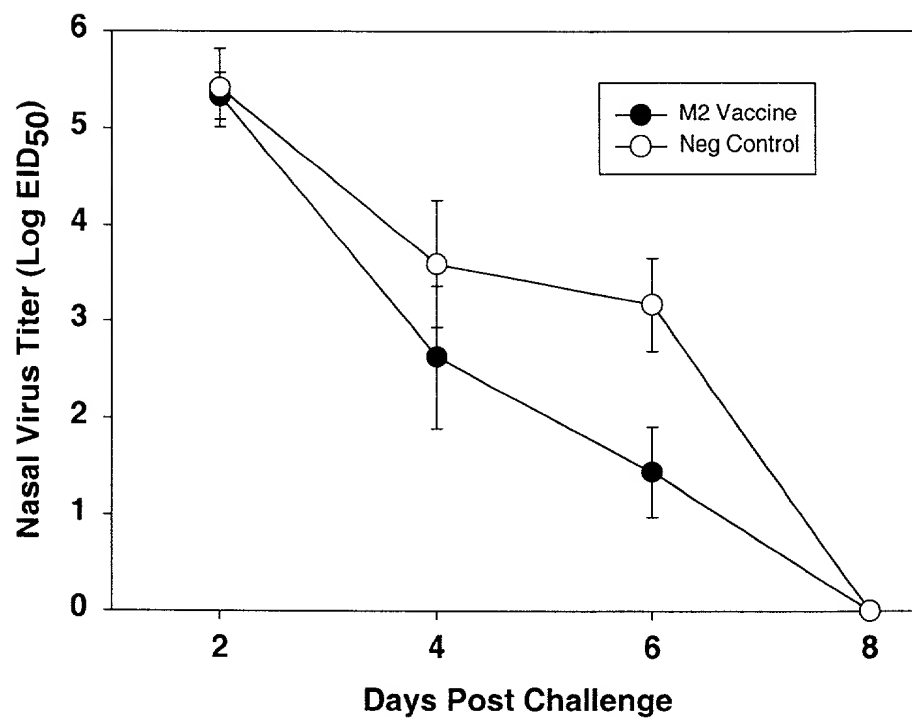


Figure 5